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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/775,964

DATE: 08/16/2002  
TIME: 10:29:57

Input Set : N:\Crf3\RULE60\09775964.raw  
Output Set: N:\CRF4\08162002\I775964.raw

## SEQUENCE LISTING

## 1 (1) GENERAL INFORMATION:

(i) APPLICANT: Asada, Kiyozo  
Uemori, Takashi  
Ueno, Takashi  
Koyama, Nobuto  
Hashino, Kimikazu  
Kato, Ikunoshin

ENTERED

(ii) TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET  
CELLS WITH RETROVIRUS

(iii) NUMBER OF SEQUENCES: 39

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: WEISER & ASSOCIATES  
(B) STREET: 230 South Fifteenth Street, Suite 500  
(C) CITY: Philadelphia  
(D) STATE: PA  
(E) COUNTRY: USA  
(F) ZIP: 19102

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/775,964  
(B) FILING DATE: 20-Feb-2001  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/366,009  
(B) FILING DATE: 02-Aug-1999  
(A) APPLICATION NUMBER: 08/809,156  
(B) FILING DATE:  
(A) APPLICATION NUMBER: JP 294382/1995  
(B) FILING DATE: 13-NOV-1995  
(A) APPLICATION NUMBER: JP 051847/1996  
(B) FILING DATE: 08-MAR-1996

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Weiser, Gerard J.  
(B) REGISTRATION NUMBER: 19,763  
(C) REFERENCE/DOCKET NUMBER: 977.6507P

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 215-875-8383  
(B) TELEFAX: 215-875-8394

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## 43 (2) INFORMATION FOR SEQ ID NO: 1:

## 44 (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 271 amino acids

46 (B) TYPE: amino acid

47 (C) STRANDEDNESS:

48 (D) TOPOLOGY: linear

## 49 (ii) MOLECULE TYPE: peptide

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

51   Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr
52   1           5           10           15
53   Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr
54           20           25           30
55   Arg Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile
56           35           40           45
57   Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val
58           50           55           60
59   Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr
60   65           70           75           80
61   Ser Arg Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro
62           85           90           95
63   Pro Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile
64           100          105          110
65   Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala
66           115          120          125
67   Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp
68           130          135          140
69   Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys
70   145          150          155          160
71   Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val
72           165          170          175
73   Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu
74           180          185          190
75   Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala
76           195          200          205
77   Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro
78           210          215          220
79   Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile
80   225          230          235          240
81   Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu
82           245          250          255
83   Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr
84           260          265          270

```

## 86 (2) INFORMATION FOR SEQ ID NO: 2:

## 87 (i) SEQUENCE CHARACTERISTICS:

88 (A) LENGTH: 25 amino acids

89 (B) TYPE: amino acid

90 (C) STRANDEDNESS:

91 (D) TOPOLOGY: linear

## 92 (ii) MOLECULE TYPE: peptide

## RAW SEQUENCE LISTING

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```

93      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
94      Asp Glu Leu Pro Gln Leu Val Thr Leu Pro His Pro Asn Leu His Gly
95      1              5              10              15
96      Pro Glu Ile Leu Asp Val Pro Ser Thr
97      20              25
99 (2) INFORMATION FOR SEQ ID NO: 3:
100      (i) SEQUENCE CHARACTERISTICS:
101          (A) LENGTH: 155 amino acids
102          (B) TYPE: amino acid
103          (C) STRANDEDNESS:
104          (D) TOPOLOGY: linear
105      (ii) MOLECULE TYPE: peptide
106      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
107      Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
108      1              5              10              15
109      Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
110      20              25              30
111      Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
112      35              40              45
113      Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
114      50              55              60
115      Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
116      65              70              75              80
117      Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
118      85              90              95
119      Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
120      100              105              110
121      Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
122      115              120              125
123      Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
124      130              135              140
125      Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
126      145              150              155
128 (2) INFORMATION FOR SEQ ID NO: 4:
129      (i) SEQUENCE CHARACTERISTICS:
130          (A) LENGTH: 432 amino acids
131          (B) TYPE: amino acid
132          (C) STRANDEDNESS:
133          (D) TOPOLOGY: linear
134      (ii) MOLECULE TYPE: peptide
135      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
136      Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg Val
137      1              5              10              15
138      Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu Val Arg
139      20              25              30
140      Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu Ser Ile Ser
141      35              40              45
142      Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu Pro Gly Thr Glu
143      50              55              60

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144	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	Tyr	Glu	Gln	His	Glu	Ser	Thr	Pro
145	65					70					75					80
146	Leu	Arg	Gly	Arg	Gln	Lys	Thr	Gly	Leu	Asp	Ser	Pro	Thr	Gly	Ile	Asp
147					85					90					95	
148	Phe	Ser	Asp	Ile	Thr	Ala	Asn	Ser	Phe	Thr	Val	His	Trp	Ile	Ala	Pro
149				100					105					110		
150	Arg	Ala	Thr	Ile	Thr	Gly	Tyr	Arg	Ile	Arg	His	His	Pro	Glu	His	Phe
151			115					120					125			
152	Ser	Gly	Arg	Pro	Arg	Glu	Asp	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile
153		130					135					140				
154	Thr	Leu	Thr	Asn	Leu	Thr	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val
155	145					150					155					160
156	Ala	Leu	Asn	Gly	Arg	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln	Gln	Ser
157				165						170					175	
158	Thr	Val	Ser	Asp	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro
159			180						185						190	
160	Thr	Ser	Leu	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val	Thr	Val	Arg	Tyr
161		195						200						205		
162	Tyr	Arg	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val	Gln	Glu
163		210				215						220				
164	Phe	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala	Thr	Ile	Ser	Gly	Leu	Lys
165	225				230						235					240
166	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val	Thr	Gly	Arg	Gly
167				245						250					255	
168	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro	Ile	Ser	Ile	Asn	Tyr	Arg	Thr	Glu
169			260						265					270		
170	Ile	Asp	Lys	Pro	Ser	Met	Ala	Ala	Gly	Ser	Ile	Thr	Thr	Leu	Pro	Ala
171		275						280					285			
172	Leu	Pro	Glu	Asp	Gly	Gly	Ser	Gly	Ala	Phe	Pro	Pro	Gly	His	Phe	Lys
173		290					295					300				
174	Asp	Pro	Lys	Arg	Leu	Tyr	Cys	Lys	Asn	Gly	Gly	Phe	Phe	Leu	Arg	Ile
175	305				310						315					320
176	His	Pro	Asp	Gly	Arg	Val	Asp	Gly	Val	Arg	Glu	Lys	Ser	Asp	Pro	His
177				325						330					335	
178	Ile	Lys	Leu	Gln	Leu	Gln	Ala	Glu	Glu	Arg	Gly	Val	Val	Ser	Ile	Lys
179			340						345					350		
180	Gly	Val	Cys	Ala	Asn	Arg	Tyr	Leu	Ala	Met	Lys	Glu	Asp	Gly	Arg	Leu
181		355						360					365			
182	Leu	Ala	Ser	Lys	Cys	Val	Thr	Asp	Glu	Cys	Phe	Phe	Phe	Glu	Arg	Leu
183		370					375						380			
184	Glu	Ser	Asn	Asn	Tyr	Asn	Thr	Tyr	Arg	Ser	Arg	Lys	Tyr	Thr	Ser	Trp
185	385				390						395					400
186	Tyr	Val	Ala	Leu	Lys	Arg	Thr	Gly	Gln	Tyr	Lys	Leu	Gly	Ser	Lys	Thr
187				405						410					415	
188	Gly	Pro	Gly	Gln	Lys	Ala	Ile	Leu	Phe	Leu	Pro	Met	Ser	Ala	Lys	Ser
189			420						425					430		

191 (2) INFORMATION FOR SEQ ID NO: 5:

192 (i) SEQUENCE CHARACTERISTICS:

193 (A) LENGTH: 457 amino acids

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194      (B) TYPE: amino acid
195      (C) STRANDEDNESS:
196      (D) TOPOLOGY: linear
197      (ii) MOLECULE TYPE: peptide
198      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
199      Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg Val
200      1          5          10          15
201      Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu Val Arg
202      20          25          30
203      Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu Ser Ile Ser
204      35          40          45
205      Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu Pro Gly Thr Glu
206      50          55          60
207      Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln His Glu Ser Thr Pro
208      65          70          75          80
209      Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp Ser Pro Thr Gly Ile Asp
210      85          90          95
211      Phe Ser Asp Ile Thr Ala Asn Ser Phe Thr Val His Trp Ile Ala Pro
212      100         105         110
213      Arg Ala Thr Ile Thr Gly Tyr Arg Ile Arg His His Pro Glu His Phe
214      115         120         125
215      Ser Gly Arg Pro Arg Glu Asp Arg Val Pro His Ser Arg Asn Ser Ile
216      130         135         140
217      Thr Leu Thr Asn Leu Thr Pro Gly Thr Glu Tyr Val Val Ser Ile Val
218      145         150         155         160
219      Ala Leu Asn Gly Arg Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser
220      165         170         175         180
221      Thr Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
222      180         185         190
223      Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr
224      195         200         205
225      Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
226      210         215         220
227      Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys
228      225         230         235         240
229      Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg Gly
230      245         250         255
231      Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr Glu
232      260         265         270
233      Ile Asp Lys Pro Ser Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala
234      275         280         285
235      Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys
236      290         295         300
237      Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile
238      305         310         315         320
239      His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His
240      325         330         335
241      Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys
242      340         345         350

```

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/775,964

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Input Set : N:\Crf3\RULE60\09775964.raw  
Output Set: N:\CRF4\08162002\I775964.raw

L:24 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:25 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:435 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:445 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10  
L:455 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11  
L:465 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12  
L:667 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15  
L:677 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16  
L:687 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17  
L:724 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18  
L:734 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19  
L:744 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20  
L:1135 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26  
L:1167 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27  
L:1343 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31  
L:1353 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32  
L:1363 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33  
L:1462 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35  
L:1472 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36  
L:1482 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37  
L:1492 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=38  
L:1502 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=39